SEQUENCE LISTING

<110> Elixir Pharmaceuticals, Inc.

<120> SIRT1 AND GENETIC DISORDERS

<130> 13407-039WO1

<150> US 60/484,327
<151> 2003-07-02

<160> 3

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Ala Asp Glu Ala Ala Leu Ala Leu Gln Pro Gly Gly Ser Pro Ser Ala
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gcg ggg gcc gac agg gag gcc gcg tcg tcc ccc gcc ggg gag ccg ctc          152
Ala Gly Ala Asp Arg Glu Ala Ala Ser Ser Pro Ala Gly Glu Pro Leu
            20                  25                  30

cgc aag agg ccg cgg aga gat ggt ccc ggc ctc gag cgg agc ccg ggc          200
Arg Lys Arg Pro Arg Arg Asp Gly Pro Gly Leu Glu Arg Ser Pro Gly
        35                  40                  45

gag ccc ggt ggg gcg gcc cca gag cgt gag gtg ccg gcg gcg gcc agg          248
Glu Pro Gly Gly Ala Ala Pro Glu Arg Glu Val Pro Ala Ala Ala Arg
50                  55                  60                  65

ggc tgc ccg ggt gcg gcg gcg gcg gcg ctg tgg cgg gag gcg gag gca          296
Gly Cys Pro Gly Ala Ala Ala Ala Ala Leu Trp Arg Glu Ala Glu Ala
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gag gcg gcg gcg gca ggc ggg gag caa gag gcc cag gcg act gcg gcg          344
Glu Ala Ala Ala Ala Gly Gly Glu Gln Glu Ala Gln Ala Thr Ala Ala
                85                  90                  95

gct ggg gaa gga gac aat ggg ccg ggc ctg cag ggc cca tct cgg gag          392
Ala Gly Glu Gly Asp Asn Gly Pro Gly Leu Gln Gly Pro Ser Arg Glu
            100                 105                 110

cca ccg ctg gcc gac aac ttg tac gac gaa gac gac gac gac gag ggc          440
Pro Pro Leu Ala Asp Asn Leu Tyr Asp Glu Asp Asp Asp Asp Glu Gly
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            115                    120                    125
gag gag gag gaa gag gcg gcg gcg gcg gcg att ggg tac cga gat aac    488
Glu Glu Glu Glu Glu Ala Ala Ala Ala Ala Ile Gly Tyr Arg Asp Asn
130          135              140              145

ctt ctg ttc ggt gat gaa att atc act aat ggt ttt cat tcc tgt gaa    536
Leu Leu Phe Gly Asp Glu Ile Ile Thr Asn Gly Phe His Ser Cys Glu
            150              155              160

agt gat gag gag gat aga gcc tca cat gca agc tct agt gac tgg act    584
Ser Asp Glu Glu Asp Arg Ala Ser His Ala Ser Ser Ser Asp Trp Thr
            165              170              175

cca agg cca cgg ata ggt cca tat act ttt gtt cag caa cat ctt atg    632
Pro Arg Pro Arg Ile Gly Pro Tyr Thr Phe Val Gln Gln His Leu Met
            180              185              190

att ggc aca gat cct cga aca att ctt aaa gat tta ttg ccg gaa aca    680
Ile Gly Thr Asp Pro Arg Thr Ile Leu Lys Asp Leu Leu Pro Glu Thr
        195              200              205

ata cct cca cct gag ttg gat gat atg aca ctg tgg cag att gtt att    728
Ile Pro Pro Pro Glu Leu Asp Asp Met Thr Leu Trp Gln Ile Val Ile
210              215              220              225

aat atc ctt tca gaa cca cca aaa agg aaa aaa aga aaa gat att aat    776
Asn Ile Leu Ser Glu Pro Pro Lys Arg Lys Lys Arg Lys Asp Ile Asn
            230              235              240

aca att gaa gat gct gtg aaa tta ctg caa gag tgc aaa aaa att ata    824
Thr Ile Glu Asp Ala Val Lys Leu Leu Gln Glu Cys Lys Lys Ile Ile
            245              250              255

gtt cta act gga gct ggg gtg tct gtt tca tgt gga ata cct gac ttc    872
Val Leu Thr Gly Ala Gly Val Ser Val Ser Cys Gly Ile Pro Asp Phe
        260              265              270

agg tca agg gat ggt att tat gct cgc ctt gct gta gac ttc cca gat    920
Arg Ser Arg Asp Gly Ile Tyr Ala Arg Leu Ala Val Asp Phe Pro Asp
275              280              285

ctt cca gat cct caa gcg atg ttt gat att gaa tat ttc aga aaa gat    968
Leu Pro Asp Pro Gln Ala Met Phe Asp Ile Glu Tyr Phe Arg Lys Asp
290              295              300              305

cca aga cca ttc ttc aag ttt gca aag gaa ata tat cct gga caa ttc   1016
Pro Arg Pro Phe Phe Lys Phe Ala Lys Glu Ile Tyr Pro Gly Gln Phe
            310              315              320

cag cca tct ctc tgt cac aaa ttc ata gcc ttg tca gat aag gaa gga   1064
Gln Pro Ser Leu Cys His Lys Phe Ile Ala Leu Ser Asp Lys Glu Gly
            325              330              335

aaa cta ctt cgc aac tat acc cag aac ata gac acg ctg gaa cag gtt   1112
Lys Leu Leu Arg Asn Tyr Thr Gln Asn Ile Asp Thr Leu Glu Gln Val
        340              345              350

gcg gga atc caa agg ata att cag tgt cat ggt tcc ttt gca aca gca   1160
Ala Gly Ile Gln Arg Ile Ile Gln Cys His Gly Ser Phe Ala Thr Ala
        355              360              365
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tct tgc ctg att tgt aaa tac aaa gtt gac tgt gaa gct gta cga gga    1208
Ser Cys Leu Ile Cys Lys Tyr Lys Val Asp Cys Glu Ala Val Arg Gly
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gat att ttt aat cag gta gtt cct cga tgt cct agg tgc cca gct gat    1256
Asp Ile Phe Asn Gln Val Val Pro Arg Cys Pro Arg Cys Pro Ala Asp
                390             395             400

gaa ccg ctt gct atc atg aaa cca gag att gtg ttt ttt ggt gaa aat    1304
Glu Pro Leu Ala Ile Met Lys Pro Glu Ile Val Phe Phe Gly Glu Asn
            405             410             415

tta cca gaa cag ttt cat aga gcc atg aag tat gac aaa gat gaa gtt    1352
Leu Pro Glu Gln Phe His Arg Ala Met Lys Tyr Asp Lys Asp Glu Val
        420             425             430

gac ctc ctc att gtt att ggg tct tcc ctc aaa gta aga cca gta gca    1400
Asp Leu Leu Ile Val Ile Gly Ser Ser Leu Lys Val Arg Pro Val Ala
    435             440             445

cta att cca agt tcc ata ccc cat gaa gtg cct cag ata tta att aat    1448
Leu Ile Pro Ser Ser Ile Pro His Glu Val Pro Gln Ile Leu Ile Asn
450             455             460             465

aga gaa cct ttg cct cat ctg cat ttt gat gta gag ctt ctt gga gac    1496
Arg Glu Pro Leu Pro His Leu His Phe Asp Val Glu Leu Leu Gly Asp
            470             475             480

tgt gat gtc ata att aat gaa ttg tgt cat agg tta ggt ggt gaa tat    1544
Cys Asp Val Ile Ile Asn Glu Leu Cys His Arg Leu Gly Gly Glu Tyr
            485             490             495

gcc aaa ctt tgc tgt aac cct gta aag ctt tca gaa att act gaa aaa    1592
Ala Lys Leu Cys Cys Asn Pro Val Lys Leu Ser Glu Ile Thr Glu Lys
        500             505             510

cct cca cga aca caa aaa gaa ttg gct tat ttg tca gag ttg cca ccc    1640
Pro Pro Arg Thr Gln Lys Glu Leu Ala Tyr Leu Ser Glu Leu Pro Pro
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aca cct ctt cat gtt tca gaa gac tca agt tca cca gaa aga act tca    1688
Thr Pro Leu His Val Ser Glu Asp Ser Ser Ser Pro Glu Arg Thr Ser
530             535             540             545

cca cca gat tct tca gtg att gtc aca ctt tta gac caa gca gct aag    1736
Pro Pro Asp Ser Ser Val Ile Val Thr Leu Leu Asp Gln Ala Ala Lys
            550             555             560

agt aat gat gat tta gat gtg tct gaa tca aaa ggt tgt atg gaa gaa    1784
Ser Asn Asp Asp Leu Asp Val Ser Glu Ser Lys Gly Cys Met Glu Glu
            565             570             575

aaa cca cag gaa gta caa act tct agg aat gtt gaa agt att gct gaa    1832
Lys Pro Gln Glu Val Gln Thr Ser Arg Asn Val Glu Ser Ile Ala Glu
        580             585             590

cag atg gaa aat ccg gat ttg aag aat gtt ggt tct agt act ggg gag    1880
Gln Met Glu Asn Pro Asp Leu Lys Asn Val Gly Ser Ser Thr Gly Glu
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aaa aat gaa aga act tca gtg gct gga aca gtg aga aaa tgc tgg cct      1928
Lys Asn Glu Arg Thr Ser Val Ala Gly Thr Val Arg Lys Cys Trp Pro
610             615             620             625

aat aga gtg gca aag gag cag att agt agg cgg ctt gat ggt aat cag      1976
Asn Arg Val Ala Lys Glu Gln Ile Ser Arg Arg Leu Asp Gly Asn Gln
                630             635             640

tat ctg ttt ttg cca cca aat cgt tac att ttc cat ggc gct gag gta      2024
Tyr Leu Phe Leu Pro Pro Asn Arg Tyr Ile Phe His Gly Ala Glu Val
            645             650             655

tat tca gac tct gaa gat gac gtc tta tcc tct agt tct tgt ggc agt      2072
Tyr Ser Asp Ser Glu Asp Asp Val Leu Ser Ser Ser Ser Cys Gly Ser
        660             665             670

aac agt gat agt ggg aca tgc cag agt cca agt tta gaa gaa ccc atg      2120
Asn Ser Asp Ser Gly Thr Cys Gln Ser Pro Ser Leu Glu Glu Pro Met
    675             680             685

gag gat gaa agt gaa att gaa gaa ttc tac aat ggc tta gaa gat gag      2168
Glu Asp Glu Ser Glu Ile Glu Glu Phe Tyr Asn Gly Leu Glu Asp Glu
690             695             700             705

cct gat gtt cca gag aga gct gga gga gct gga ttt ggg act gat gga      2216
Pro Asp Val Pro Glu Arg Ala Gly Gly Ala Gly Phe Gly Thr Asp Gly
            710             715             720

gat gat caa gag gca att aat gaa gct ata tct gtg aaa cag gaa gta      2264
Asp Asp Gln Glu Ala Ile Asn Glu Ala Ile Ser Val Lys Gln Glu Val
        725             730             735

aca gac atg aac tat cca tca aac aaa tca tag tgtaataatt gtgcaggtac    2317
Thr Asp Met Asn Tyr Pro Ser Asn Lys Ser *
    740             745
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cagtatattt agttttccat ttgcatgatg tttgtgtgct atagatgata ttttaaattg   3877
aaaagtttgt tttaaattat ttttacagtg aagactgttt tcagctcttt ttatattgta   3937
catagtcttt tatgtaattt actggcatat gttttgtaga ctgtttaatg actggatatc   3997
ttccttcaac ttttgaaata caaaaccagt gttttttact tgtacactgt tttaaagtct   4057
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            20                  25                  30
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        35                  40                  45
Gly Glu Pro Gly Gly Ala Ala Pro Glu Arg Glu Val Pro Ala Ala Ala
    50                  55                  60
Arg Gly Cys Pro Gly Ala Ala Ala Ala Leu Trp Arg Glu Ala Glu
65                  70                  75                  80
Ala Glu Ala Ala Ala Ala Gly Gly Glu Gln Glu Ala Gln Ala Thr Ala
                85                  90                  95
Ala Ala Gly Glu Gly Asp Asn Gly Pro Gly Leu Gln Gly Pro Ser Arg
            100                 105                 110
Glu Pro Pro Leu Ala Asp Asn Leu Tyr Asp Glu Asp Asp Asp Glu
        115                 120                 125
Gly Glu Glu Glu Glu Glu Ala Ala Ala Ala Ile Gly Tyr Arg Asp
    130                 135                 140
Asn Leu Leu Phe Gly Asp Glu Ile Ile Thr Asn Gly Phe His Ser Cys
145                 150                 155                 160
Glu Ser Asp Glu Glu Asp Arg Ala Ser His Ala Ser Ser Ser Asp Trp
                165                 170                 175
Thr Pro Arg Pro Arg Ile Gly Pro Tyr Thr Phe Val Gln Gln His Leu
            180                 185                 190
Met Ile Gly Thr Asp Pro Arg Thr Ile Leu Lys Asp Leu Leu Pro Glu
        195                 200                 205
Thr Ile Pro Pro Pro Glu Leu Asp Asp Met Thr Leu Trp Gln Ile Val
    210                 215                 220
Ile Asn Ile Leu Ser Glu Pro Pro Lys Arg Lys Lys Arg Lys Asp Ile
225                 230                 235                 240
Asn Thr Ile Glu Asp Ala Val Lys Leu Leu Gln Glu Cys Lys Lys Ile
                245                 250                 255
Ile Val Leu Thr Gly Ala Gly Val Ser Val Ser Cys Gly Ile Pro Asp
            260                 265                 270
Phe Arg Ser Arg Asp Gly Ile Tyr Ala Arg Leu Ala Val Asp Phe Pro
        275                 280                 285
Asp Leu Pro Asp Pro Gln Ala Met Phe Asp Ile Glu Tyr Phe Arg Lys
    290                 295                 300
Asp Pro Arg Pro Phe Phe Lys Phe Ala Lys Glu Ile Tyr Pro Gly Gln
305                 310                 315                 320
Phe Gln Pro Ser Leu Cys His Lys Phe Ile Ala Leu Ser Asp Lys Glu
                325                 330                 335
Gly Lys Leu Leu Arg Asn Tyr Thr Gln Asn Ile Asp Thr Leu Glu Gln
            340                 345                 350
Val Ala Gly Ile Gln Arg Ile Ile Gln Cys His Gly Ser Phe Ala Thr
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Ala Ser Cys Leu Ile Cys Lys Tyr Lys Val Asp Cys Glu Ala Val Arg
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Gly Asp Ile Phe Asn Gln Val Val Pro Arg Cys Pro Arg Cys Pro Ala
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Asp Glu Pro Leu Ala Ile Met Lys Pro Glu Ile Val Phe Phe Gly Glu
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Asn Leu Pro Glu Gln Phe His Arg Ala Met Lys Tyr Asp Lys Asp Glu
                420                      425                      430
Val Asp Leu Leu Ile Val Ile Gly Ser Ser Leu Lys Val Arg Pro Val
            435                      440                      445
Ala Leu Ile Pro Ser Ser Ile Pro His Glu Val Pro Gln Ile Leu Ile
        450                      455                      460
Asn Arg Glu Pro Leu Pro His Leu His Phe Asp Val Glu Leu Leu Gly
    465                      470                      475                      480
Asp Cys Asp Val Ile Ile Asn Glu Leu Cys His Arg Leu Gly Gly Glu
                    485                      490                      495
Tyr Ala Lys Leu Cys Cys Asn Pro Val Lys Leu Ser Glu Ile Thr Glu
                500                      505                      510
Lys Pro Pro Arg Thr Gln Lys Glu Leu Ala Tyr Leu Ser Glu Leu Pro
            515                      520                      525
Pro Thr Pro Leu His Val Ser Glu Asp Ser Ser Ser Pro Glu Arg Thr
        530                      535                      540
Ser Pro Pro Asp Ser Ser Val Ile Val Thr Leu Leu Asp Gln Ala Ala
    545                      550                      555                      560
Lys Ser Asn Asp Asp Leu Asp Val Ser Glu Ser Lys Gly Cys Met Glu
                565                      570                      575
Glu Lys Pro Gln Glu Val Gln Thr Ser Arg Asn Val Glu Ser Ile Ala
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Glu Gln Met Glu Asn Pro Asp Leu Lys Asn Val Gly Ser Ser Thr Gly
        595                      600                      605
Glu Lys Asn Glu Arg Thr Ser Val Ala Gly Thr Val Arg Lys Cys Trp
    610                      615                      620
Pro Asn Arg Val Ala Lys Glu Gln Ile Ser Arg Arg Leu Asp Gly Asn
625                      630                      635                          640
Gln Tyr Leu Phe Leu Pro Pro Asn Arg Tyr Ile Phe His Gly Ala Glu
                645                      650                      655
Val Tyr Ser Asp Ser Glu Asp Asp Val Leu Ser Ser Ser Ser Cys Gly
            660                      665                      670
Ser Asn Ser Asp Ser Gly Thr Cys Gln Ser Pro Ser Leu Glu Glu Pro
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Met Glu Asp Glu Ser Glu Ile Glu Glu Phe Tyr Asn Gly Leu Glu Asp
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Glu Pro Asp Val Pro Glu Arg Ala Gly Gly Ala Gly Phe Gly Thr Asp
705                      710                      715                          720
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